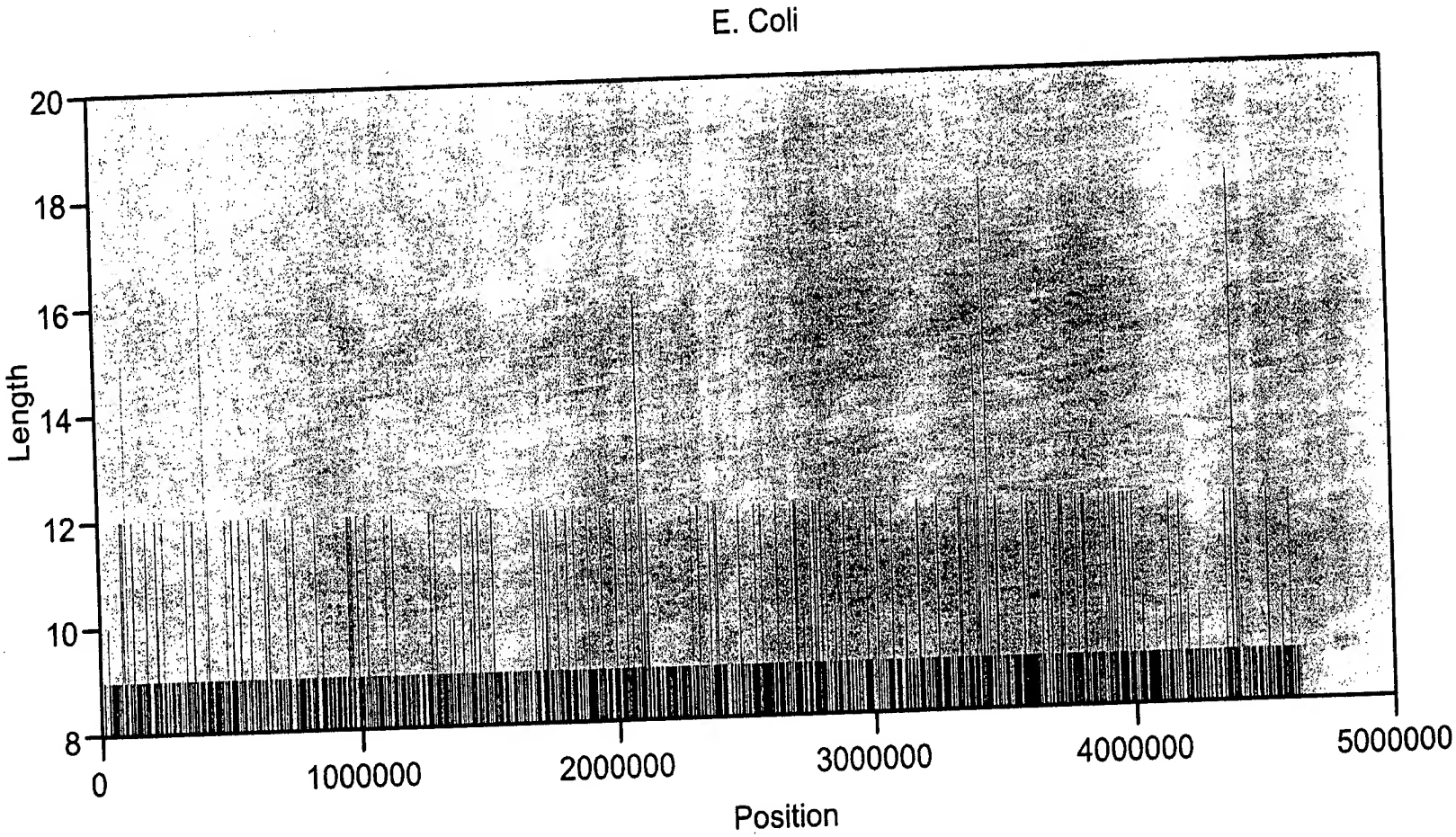
E. Coli
Length
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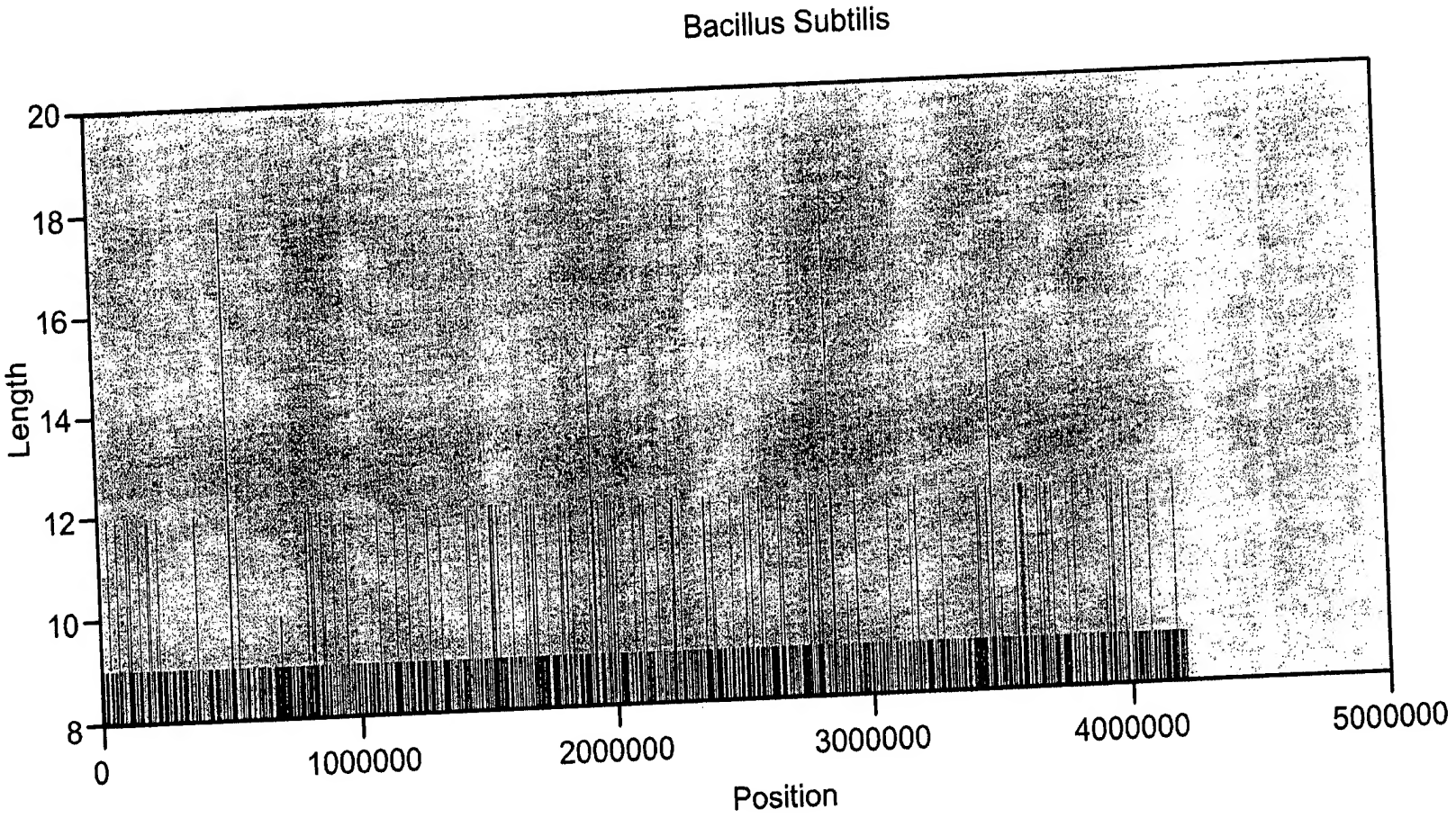
18
16
14
12
10
8
0
1000000
2000000
3000000
4000000
5000000
Position

Fig. 1a


Bacillus Subtilis
Length
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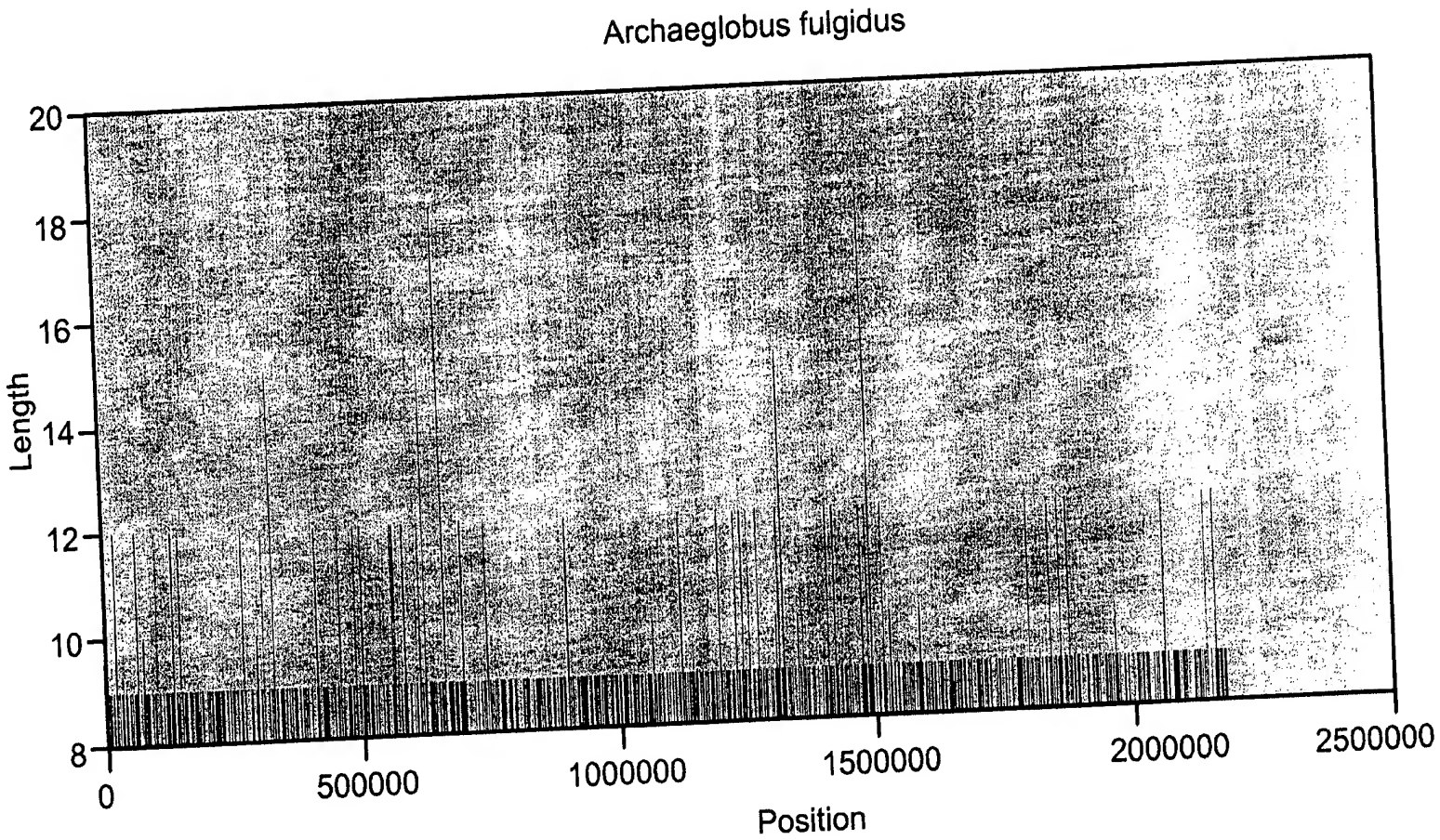
18
16
14
12
10
8
0
1000000
2000000
3000000
4000000
5000000
Position

Fig. 1b


Archaeglobus fulgidus
Length
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18
16
14
12
10
8
0
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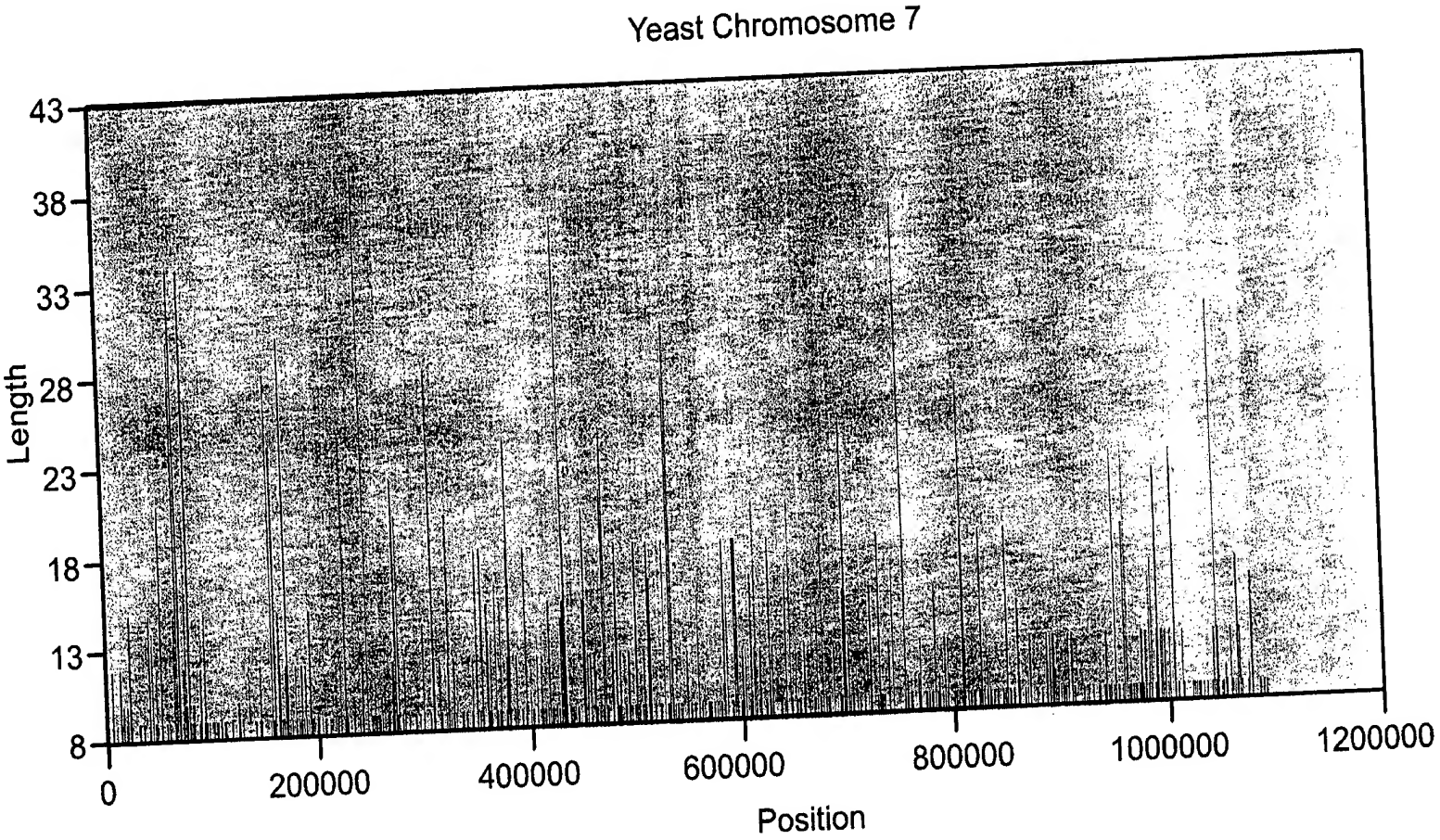
1000000
1500000
2000000
2500000
Position

Fig. 1c


Yeast Chromosome 7
Length
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33
28
23
18
13
8
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400000
600000
800000
1000000
1200000
Position

Fig. 1d

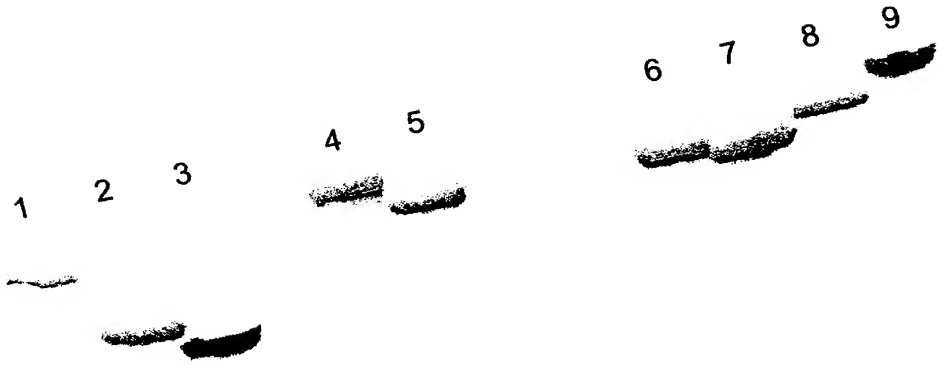

Fig. 2

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                                                                    50
                    1
Ec K12, DH5α        ~~~GTTATGT CTTATCCCAC GGTATTTAAT ATGGTTCATT AGGATGTTTA 25*
Ec Bsr9b            ~TTGTTATGT CTTATCCCAC GGTATTTAAT ATAGTTCATT TGGATGTTCA 26*
Ec Bsr9c            TTTGTTATGT CTTATCCCAC GGTATTTAAT ATAGTTCATT TGGATGTTCA 27*
Ec ETEC             ~TCTATGTTC TTATCNCCAC GGTNTTTAAT ATGGTtCATT AGGATGTTTA 28*

        Consensus   -----T-T-- -T---CCCAC GGTATTTAAT AT-GTTCATT -GGATGTT-A 29*

                                                                   100
                    51
Ec K12, DH5α        TTTCTTGATT TTGCATATGA GTATATTA.. CCCCCCCCTC AAAAAAATAA
Ec Bsr9b            TTTCTTTATT TTGCATATGA GTATATTA.. ....CCCCTT CAAAAAATAA
Ec Bsr9c            TTTCTTTATT TTGCATATGA GTATATTA.. ....CCCCTT CAAAAAATAA
Ec ETEC             TTTCTTGATT TTGCATATGA GTATATTACC CCCCCCCCTC AAAAAAATAA

        Consensus   TTTCTT-ATT TTGCATATGA GTATATTA-- ----CCCCT- -AAAAAATAA

                                                                   150
                    101
Ec K12, DH5α        ATTAATTAAA ATGATGGCTT ATATAAAATA AAATTTAAAG CAAGGAATCT
Ec Bsr9b            ATTAATTAAA ACGATTGCTT ATATAAAACA AAATTTAAAG CAAGGAATCT
Ec Bsr9c            ATTAATTAAA ACGATTGCTT ATATAAAACA AAATTTAAAG CAAGGAATCT
Ec ETEC             ATTAATTAAA ATGATGGCTT ATATNAAATA NAATTTAAAG CAAGGANTCT

        Consensus   ATTAATTAAA A-GAT-GCTT ATATAAAA-A AAATTTAAAG CAAGGAATCT

                                                                   200
                    151
Ec K12, DH5α        CAATGGATGT TAAACAAAAT GAGATTTTGT GAAAGCAATA AATTATTGAC
Ec Bsr9b            CAATGGATGT TAAACAAAAT GAGATTTAGT GAAAACAATA AATTATTCAC
Ec Bsr9c            CAATGGATGT TAAACAAAAT GAGATTTAGT GAAAACAATA AATTATTCAC
Ec ETEC             CAATGGATGT TAAACANAAT GAGATTTTGT GAANGCNATN NATTATTGNC

        Consensus   CAATGGATGT TAAACAAAAT GAGATTT-GT GAAA-CAATA AATTATT-AC

                                                                   250
                    201
Ec K12, DH5α        TTCGTTTTAG ATTTGTTTAG CTATAATGTT ATACATTCAA ATGACTGAAC
Ec Bsr9b            TTCGTTTTAG ATTTGTTTAG CTATAATGTT ATACATTCAA ATGACTGAAC
Ec Bsr9c            TTCGTTTTAG ATTTGTTTAG CTATAATGTT ATACATTCAA ATGACTGAAC
Ec ETEC             TTCGTTGTAN ATTTGCTNAG CTATAATGTT ATNCATTCAA ATGACTGAAC

        Consensus   TTCGTT-TAG ATTTG-TTAG CTATAATGTT ATACATTCAA ATGACTGAAC

                    251         264
Ec K12  DH5α        ATCCTGTAAT TAAA
Ec Bsr9b            ATCCTGTATT TAA~
Ec Bsr9c            ATCCTGTAAT TAA~
Ec ETEC             ATCCTGTNNT TANA

        Consensus   ATCCTGTAAT TAA~
```

* SEQ ID NO

Fig. 3a

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                    1                                                  50
Ec K12, DH5α        TTTNCCCGGA AAAAAATAGG AAAGGGGGGG GGGCTAATCG GCAGGGAAGG 30*
Ec K12, w3110       TNTTNNNCGG AAAAAAATNG AAAGGGGGGG GGGCTAATCG GCAGGGAAGG 31*
Ec Bsr9c            --TTTNCCGG AAAAAAATNG AAA..GGGGG GGGCTAATCG GCAGGGAAGG 32*
Ec (wt) 1           --TNTNCGGA AAAAAANAGG AAAGGGGGGG GGGCTAATCG GCAGGGAAGG 33*
Ec (wt) 54          --------NCG GAAAAAAATG AAA.GGGGGG GGGCTAATCG GCAGGGAAGG 34*
Ec (wt) 68          ---------CG GAAAAAAATG AAA.GGGGGG GGGCTAATCG GCAGGGAAGG 35*

      Consensus     ---------- -AAAAAA--G AAA--GGGGG GGGCTAATCG GCAGGGAAGG 36*

                    51                                                 100
Ec K12, DH5α        CCGCCCCGGA TAGCGGGCGG CANAAGGAAT CANAATTTCC AGGTCAGACG
Ec K12, w3110       CCGCCCCGGA TAGCGGGCGG CAGAAGGAAT CAGAATTTCC AGGTCAGACG
Ec Bsr9c            CCGCCCCGGA TAGCGGGCGG CAGAAGGAAT CAGAATTTCC AGGTCAGATG
Ec (wt) 1           CCGCCCCGGA TAGCGGGCGG CAGAAGGAAT CAGAATTTCC AGGTCAGACG
Ec (wt) 54          CCGCCCCGGA TAGCGGGCGG CAGAAGGAAT CAGAATTTCC AGGTCAGATG
Ec (wt) 68          CCGCCCCGGA TAGCGGGCGG CAGAAGGAAT CAGAATTTCC AGGTCAGATG

      Consensus     CCGCCCCGGA TAGCGGGCGG CAGAAGGAAT CAGAATTTCC AGGTCAGA-G

                    101                                                150
Ec K12,DH5α         GGCTGCAAGT TGCAGACCGT TAAAATCATC GGNNGGGGTG TCGTACCACA
Ec K12, w3110       GGCTGCAAGT TGCAGACCGT TAAAATCATC GGTTGGGGTG TCGTACCACA
Ec Bsr9c            GGCTGCAAGT TGCAGACCGT TATAATCATC GGTTGGGGTG TCGTACCACA
Ec (wt) 1           GGCTGCAAGT TGCAGACCGT TAAAATCATC GGTTGGGGTG TCGTACCACA
Ec (wt) 54          GGCTGCAAGT TGCAGACCGT TATAATCATC GGTTGGGGTG TCGTACCACA
Ec (wt) 68          GGCTGCAAGT TGCAGACCGT TATAATCATC GGTTGGGGTG TCGTACCACA

      Consensus     GGCTGCAAGT TGCAGACCGT TA-AATCATC GGTTGGGGTG TCGTACCACA

                    151                                  180
Ec K12, DH5α        CTTTACCTGC CGTCAGCCCG AGATTAA-GTT -G
Ec K12, w3110       CTTTACCTGC CGTCAGCCCG AGATTAA-GTT -G
Ec Bsr9c            CTTTACCTGC CGTCAGCCCG AGATTAA-GTT -G
Ec (wt) 1           CTTTACCTGC CGTCAGCCCG AGATTAAAGTT TGG
Ec (wt) 54          CTTTACCTGC CGTCAGCCCG AGAT-AAAGTT TGG
Ec (wt) 68          CTTTACCTGC CGTCAGCCCG AGAT-AAAGTT TGG

      Consensus     CTTTACCTGC CGTCAGCCCG AGAT-AA-GTT -G
```

* SEQ ID NO

Fig. 3b

10

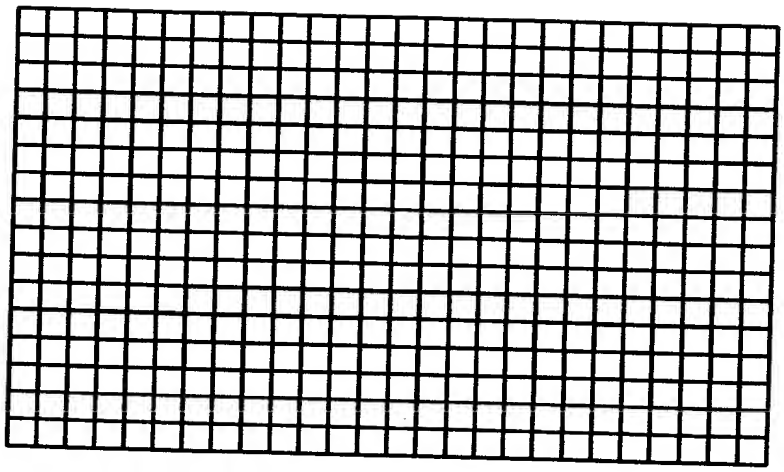

Fig. 4